

Abstract

The present invention concerns a method for investigating cytosine methylations in DNA sequences. By this means, the DNA to be investigated is reacted with a cytidine deaminase which deaminates cytidine more rapidly than 5-methylcytidine. Cytosine is converted to uracil by the conversion, whereas 5-methylcytosine remains essentially unchanged. The enzymatically pretreated DNA is preferably amplified and can be analyzed by different methods. The method according to the invention is particularly suitable for the diagnosis of cancer diseases and other disorders associated with a change in the methylation status, as well as for the prognosis of undesired drug effects.